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補正書

(54) Title : GENE SIGNATURE

(54) 発明の名称 ジーン・シグナチャー

(57) Abstract

A 3'-directed cDNA library which accurately reflects the abundance ratio of mRNA in a cell has been prepared from various human tissues, and sequencing of the cDNAs contained in the library has been conducted to examine the incidence of each cDNA in each tissue. As each cDNA has expression information with each tissue corresponding to the mRNA concentration, these cDNAs are usable as a probe or primer for detecting cell anomaly or discriminating cells. The cloned gene can produce proteins utilizable as a medicine or the like.

```
Qy   4861 agctgtcatgttggagattggtaatggctttcctgtctttgtacagttgaattcctagtc 4920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4861 AGCTGTCATGTTGGAGATTGGTAATGGCTTTCCTGTCTTTGTACAGTTGAATTCCTAGTC 4920

Qy   4921 ttccttcatccttgccctctgttggcacaggcattatctctgcaatttttagaaaatgaca 4980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4921 TTCCTTCATCCTTGCCCTCTGTTGGCACAGGCATTATCTCTGCAATTTTAGAAAATGACA 4980

Qy   4981 agtagagaatactacattgagaaactaaaccctcttcttggggtcctgatactcattccc 5040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4981 AGTAGAGAATACTACATTGAGAAACTAAACCCTCTTCTTGGGGTCCTGATACTCATTCCC 5040

Qy   5041 atttgtcccagtgctgacaacccaatcttcccaatactttcaggcctgctctacaaaagt 5100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5041 ATTTGTCCCAGTGCTGACAACCCAATCTTCCCAATACTTTCAGGCCTGCTCTACAAAAGT 5100

Qy   5101 acctgttcttgtagaaattttacagtctgccattttgggtgcccaccccaattttttacct 5160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5101 ACCTGTTCTTGTAGAAATTTTACAGTCTGCCATTTTGGGTGCCCACCCCAATTTTTACCT 5160

Qy   5161 tttagtaagttggcatgaaatttttggtaaaatctgaaaatcacatttcagaataaaacaa 5220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5161 TTTAGTAAGTTGGCATGAAATTTTGGTAAAATCTGAAAATCACATTTCAGAATAAAACAA 5220

Qy   5221 ttgggcaaaactacctaggctttactcttgagtgtctccttttgatagggattgtttctg 5280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5221 TTGGGCAAAACTACCTAGGCTTTACTCTTGAGTGTCTCCTTTTGATAGGGATTGTTTCTG 5280

Qy   5281 gaccagtttgtctaagtcctggctcttattggttcatatgaaataatgttaacttcactt 5340
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Db   5281 GACCAGTTTGTCTAAGTCCTGGCTCTTATTGGTTCATATGAAATAATGTTAACTTCACTT 5340

Qy   5341 ctttgtatattatgtataaattagaaaatgaaaaatgtgtgaataacattgtatgaaat 5399
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5341 CTTTGTATATTATGTATAAATTAGAAAATGAAAAATGTGTGAATAACATTGTATGAAAT 5399
```

RESULT 2
T19999
ID T19999 standard; cDNA to mRNA; 322 BP.
AC T19999;
DT 17-JUL-1996 (first entry)
DE Human gene signature HUMGS01136.
KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;
KW human; cloning; mapping; non-biased library; diagnosis; detection;
KW cell typing; abnormal cell function; ss.
OS Homo sapiens.
PN WO9514772-A1.
PD 01-JUN-1995.
PF 11-NOV-1994; J01916.
PR 12-NOV-1993; JP-355504.
PA (MATS/) MATSUBARA K.
PA (OKUB/) OKUBO K.
PI Matsubara K, Okubo K;
DR WPI; 95-206931/27.
PT Identifying gene signatures in 3'-directed human cDNA library - e.g.
PT for diagnosis of abnormal cell function, by preparing cDNA that
PT reflects relative abundance of corresp. mRNA in specific human
PT tissues
PS Claim 1; Page 532; 2245pp; Japanese.
CC A single-stranded DNA (or its complementary strand or the corresp.
CC double-stranded DNA) which comprises one of the 7837 "GS" sequences
CC given in T19001-T26837 and which is able to hybridise to part of
CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
CC sequences were obtained from 3'-directed cDNA libraries prepared
CC from various human tissues; synthesis of cDNA was initiated from the
CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
CC untranslated sequence is unique to a particular mRNA species, almost
CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
CC is constructed so as to reflect accurately the relative abundance of
CC different mRNAs in the particular tissue from which it was derived.
CC The appearance frequency of a given GS in a cDNA library can be
CC determined (esp. using primers and probes derived from the GS
CC sequences) as a means of diagnosing abnormal cell function or for
CC recognising different cell types.
SQ Sequence 322 BP; 101 A; 52 C; 53 G; 111 T;

Query Match 5.8%; Score 312.4; DB 1; Length 322;
Best Local Similarity 98.1%; Pred. No. 1e-63;
Matches 313; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy   3957 gatcactttcaattgaagtcagggtattgtgcataatagaaagtattggactgagatatt 4016
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GATCACTTTCAATTGAAGTCAGGGTATTGTGCATAATAGAAAGTATTGGACTGAGATATT 60

Qy   4017 tggttaccatggaggccaatgctttttttcatcttattaaatgtgatgtgacttttttctt 4076
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db     61 TGGTTACCATGGAGGCCAATGCTTTTTTCATCTTATTAAATGTGATGTGACTTTTTNCTT 120

Qy   4077 tgtacagaagagtactgtatttttgaatagcctactcccaagtaagagcaaatctgtatg 4136
          |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TGTACACAAGAGTACTGTATTTTTGAATAGCCTACTCCCAAGTAAGAGCAAATCTGTATG 180

Qy   4137 ataacatttttttcctctggacataagacataacagtaacacgatgtacatttacaagcgg 4196
          |||||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ATAACATTTTTNCCNCTGGACATAAGACATAACAGTAACACGATGTACATTTACAAGCGG 240

Qy   4197 ccttatgtacatttcccaacaatctttttaaggcaaaattgtgaccatatgtgtataatt 4256
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db    241 CCTTATGTACATTTCCCAACANTCTTTTTAAGGCAAAATTGTGACCATATGTGTATAATT 300

Qy   4257 aaaatcgtttttaatcctt 4275
          |||||||||||||||||| |
Db    301 AAAATCGTTTTTAATCCNT 319
```

RESULT 3
T41852/c
ID T41852 standard; DNA; 9789 BP.
AC T41852;
DT 20-FEB-1997 (first entry)
DE cDNA encoding Plasmodium falciparum erythrocyte membrane protein.
KW Plasmodium falciparum; erythrocyte membrane protein; malaria;
KW detection; identification; treatment; prevention; parasite; ss.
OS Plasmodium falciparum MC type.

FH	Key	Location/Qualifiers
FT	cds	326. .9497
FT		/*tag= a
FT		/product= Erythrocyte membrane protein
FT	misc_feature	518. .520
FT		/*tag= b
FT		/transl_except= GTA encodes Tyrosine
FT	misc_feature	656. .658
FT		/*tag= c
FT		/transl_except= ATT encodes Leucine
FT	misc_feature	2909. .2911
FT		/*tag= d
FT		/transl_except= AAC encodes Aspartic acid
FT	misc_feature	3461. .3463
FT		/*tag= e
FT		/transl_except= GAA encodes Glutamine
FT	misc_feature	5546. .5548
FT		/*tag= f
FT		/transl_except= CCT encodes Arginine
FT	misc_feature	6254. .6256
FT		/*tag= g
FT		/transl_except= AAT encodes Lysine
FT	misc_feature	6257. .6259
FT		/*tag= h
FT		/transl_except= ATA encodes Tyrosine
FT	misc_feature	6263. .6265
FT		/*tag= i
FT		/transl_except= AAC encodes Lysine
FT	misc_feature	6269. .6271